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On combining wavelets expansion and sparse linear models for regression on metabolomic data and biomarker selection

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Abstract

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Wavelet thresholding of spectra has to be handled with care when the spectra are the predictors of a regression problem. Indeed, a blind thresholding of the signal followed by a regression method often leads to deteriorated predictions. The scope of this paper is to show that sparse regression methods, applied in the wavelet domain, perform an automatic thresholding: the most relevant wavelet coefficients are selected to optimize the prediction of a given target of interest. This approach can be seen as a joint thresholding designed for a predictive purpose.

The method is illustrated on a real world problem where metabolomic data is linked to poison ingestion. This example proves the usefulness of wavelet expansion and the good behavior of sparse and regularized methods. A comparison study is performed between the two-steps approach (wavelet thresholding and regression) and the one-step approach (selection of wavelet coefficients with a sparse regression). The comparison includes two types of wavelet bases, various thresholding methods and various regression methods and is evaluated by calculating prediction performances. Information about the location of the most important features on the spectra was also obtained and used to identify the most relevant metabolites involved in the mice poisoning.

1 Introduction

The recent development of high-throughput acquisition techniques in biology has brought a large amount of high dimensional data as high-resolution digitized signals. For instance, microarrays record the level of transcription of several thousands genes at the mRNA level and mass spectrometry or nuclear magnetic resonance (NMR) are used at the protein and metabolite levels. Modern biology now faces new issues related to these data: one of them is to deal with data having a high or even an extremely high dimension : typically, after a standard pre-processing, metabolomic profiles coming from NMR techniques have hundreds of variables for less than one hundred observations. In particular, the number of available samples is often much smaller than the data dimension and standard regression or classification methods are likely to overfit the data. For that reason, dimension reduction or variable selection are usually needed to improve the quality of the prediction in predictive models or to understand which features are involved in a given situation.

Dimension reduction are based on projections that usually build a small number of combinations of a large number of original features (see [Ramsay and Silverman, 1997] for examples and discussion about these approaches). Principal Component Analysis (PCA), Multidimensional scaling (MDS) [Cox and Cox, 2001] and Partial Least Squares (PLS) [Wold, 1975] are the most standard linear projection methods. Dealing with metabolomic

23 data, a commonly used basis for projecting the data is the Wavelet Trans-
 24 form (WT) [Mallat, 1999]. Wavelet expansion is frequently performed
 25 to correct the baseline and to de-noise the data by removing the small-
 26 est details with a thresholding method. Then, in a second phase, a re-
 27 gression or a classification method is applied on the thresholded signal
 28 [Xia et al., 2007, Alexandrov et al., 2009]. On the other hand, selection
 29 methods select a small number of variables among the original ones to ensure
 30 an easy interpretation, often at the cost of deteriorated prediction perfor-
 31 mances: as an example, [Wongravee et al., 2009] used a bootstrap approach
 32 and PLS-DA to select variables in a large metabolomic dataset prior a clas-
 33 sification. Finally, projection and variable selection are sometimes combined
 34 as in [Alsberg et al., 1998a, Kim et al., 2008].

35 The present paper tackles the issue of the best way to apply regression
 36 methods to metabolomic spectra. More precisely, a numerical variable of
 37 interest, that can be a phenotype or an environmental condition, is predicted
 38 from the metabolomic profile. As pointed out in [Rohart et al., 2012], the
 39 problem to predict a numerical phenotype from metabolomic data is little
 40 addressed in the literature so far, despite its numerous potential applications.
 41 Here, the focus is not merely put on achieving a good prediction accuracy but
 42 also on extracting the most influential features in the metabolomic spectra.

43 A one phase approach is tested that performs a sparse or a regularized
 44 regression method on the wavelet coefficients resulting from the wavelet rep-
 45 resentation of the spectra. Contrary to thresholding methods, where the

coefficients selection is not directly related to the prediction of the target variable, the introduced approach automatically selects the most relevant wavelet coefficients in relation to the target variable. The relevance of the proposal is assessed through a case study. The purpose is to recover the drug dose ingested by a mouse from its metabolomic profile, in order to prevent a possible illness. A comparison study is performed on this real world problem, that leads to several conclusions: first, as was expected, wavelet transform is well adapted to the representation of metabolomic data and leads to better predictive performances. Then, variable selection by a blind thresholding of the wavelet coefficients deteriorates the predictions contrary to a variable selection performed by means of a sparse approach. This last method leads to the most accurate prediction performances.

The remaining of the paper is organized as follows: Section 2 presents the case study. Section 3 briefly surveys the state-of-the-art methods used to handle metabolomic data in a regression framework and specifically focuses on wavelet preprocessing. In this section, our proposal is described as well as the methodology used for the comparison. Finally, Section 4 discusses the results and shows that the obtained regression model is relevant enough to extract interesting biomarkers related to the studied target. Some conclusions are given in Section 5.

66 2 Case study and material

67 2.1 Problem description

68 The data used in this experiment are described in [Domange et al., 2008] and
69 stand in the framework of a toxicology experiment based on metabolomic
70 data. The study is devoted to the metabolomic exploration on the mouse
71 model of the disruptive effect at the metabolic side of a plant, *Hypocho-*
72 *eris radicata* (L.) (HR), which is toxic for horse species. It may in-
73 duce severe neuropathies that bring locomotive incapacitating damages
74 [Domange et al., 2010].

75 The disruptive effect of HR is studied in male and female mice (2×36)
76 for 21 days at most. The mice were given a diet in which HR was introduced
77 in form of a ground dry powder at 3 or 9%; a control group with 12 animals
78 received no HR at all. 397 metabolomic spectra were acquired in urine, at
79 different days of the experiment. In short, the data set is $(X_i, \text{HR}_i, d_i)_{i=1, \dots, 397}$
80 where X_i is a metabolomic profile (hence a curve, as shown in Figure 1), HR_i
81 is the daily dose ingested by the corresponding mouse ($\text{HR}_i \in \{0, 3, 9\}$ and
82 d_i is the number of days from the beginning of the experiment up to the
83 spectrum acquisition ($d_i \in \{1, \dots, 21\}$). More precise information about the
84 data can be found in [Domange et al., 2010].

85 The issue of interest is to predict the total dose of HR ingested, which is
86 the daily HR dose multiplied by the number of days of ingestion, from the

87 metabolomic data. This problem can be written as a regression problem:

$$y_i = \Phi(X_i) + \epsilon_i \quad (1)$$

88 where $y_i = \text{HR}_i \times d_i$, Φ is the regression function to be estimated and ϵ_i is an
89 error term. This problem is motivated by several questions that frequently
90 arise in such an experimental settings:

- 91 • the first motivation is to know if the metabolomic profile alone is enough
92 to predict the drug dose ingested by an animal, which can be useful to
93 prevent an illness;
- 94 • conversely, the second motivation is to understand if the influence of
95 the HR dose ingestion is strong enough not to be seen as an artifact: if
96 y_i can be accurately estimated from X_i then this is a strong indication
97 that the HR dose and more precisely, its cumulative effect, is really
98 disrupting the mouse metabolomic profile;
- 99 • finally the last motivation is to use the estimated regression function
100 to corroborate a set of relevant metabolites influenced by the HR in-
101 gestion. The chosen approach is to extract the explanatory variables
102 (i.e., the part of the metabolomic profiles) with the strongest predictive
103 power, from the estimated regression function.

104 2.2 Data pre-processing

105 The data, acquired with ^1H NMR technique, are transformed as described
106 in [Domange et al., 2008] to obtain 397 spectra consisting in an intensity
107 distribution with 751 (non zero) variables. This step can be seen as a routine
108 designed to transform the original continuous signal into a discrete one, thus
109 to ease its analysis. An example of a resulting spectrum is given in Figure 1.

110 [Figure 1 about here.]

111 In order to recover the continuity of the signal, discrete wavelet decom-
112 position is performed on the pre-processed spectrum: this is one of the most
113 commonly used signal transformation approach and it is particularly well
114 suited for uneven and chaotic signals, such as metabolomic profiles. Addi-
115 tionally, the normal growth of the mice influences the metabolomic profile.
116 As this effect could be mixed with the total HR dose ingested by the mice
117 (which also depends on the day of measurement), a correction, based on
118 the control group’s quantiles alignment, is also performed on the wavelet
119 coefficients. This correction is based on the assumption that, other the con-
120 trol group, no distribution variation in the metabolomic profiles should be
121 seen: the group’s quantile alignment is a robust method leading to compa-
122 rable metabolomic profiles distributions each day, in the control group. This
123 method is quite standard in such cases (see, e.g., what is done for microarray
124 normalization in the **R** package `limma`, for instance [Bolstad et al., 2003]).

125 In the remaining, the obtained wavelet coefficients are denoted by

126 $(W_i)_{i=1,\dots,397} \subset \mathbb{R}^D$ where D is the number of wavelet coefficients used in
 127 the regression method (it depends on the wavelet basis and also on the DWT
 128 approach as described in Section 3.3 but in any case $D < 751$).

129 **3 Methodological proposal**

130 **3.1 State-of-the-art on using DWT in regression prob-** 131 **lems**

132 Wavelet transforms are often applied to signals as a pre-processing step be-
 133 fore the statistical analysis [Davis et al., 2007, Xia et al., 2007]. A threshold-
 134 ing approach on the discrete wavelet transform is then generally performed
 135 in order to remove the smallest (and most irrelevant) detailed coefficients
 136 from the spectra representation. Standard thresholding strategies are the
 137 so-called “hard thresholding” that simply removes the smallest coefficients
 138 and leaves the others unchanged and the “soft thresholding” that removes
 139 the coefficients smaller than a given threshold and reduces the others from
 140 the value of this threshold. Of course, the choice of the threshold is very
 141 important and several solutions have been proposed: for instance, the SURE
 142 and Universal policies are calculated from an estimation of the level of noise
 143 and justified by asymptotic properties (see [Donoho and Johnstone, 1994,
 144 Donoho, 1995, Donoho and Johnstone, 1995, Donoho et al., 1995]). Also,
 145 [Nason, 1996] suggests to use a cross-validation criterion to choose the thresh-

old and [Johnstone and Silverman, 1997] to rely on a different threshold for each level. More recently, [González et al., 2013] shows that keeping solely the finest details coefficients at the lowest decomposition level produces a representation of the data having the ability to correct a putative baseline default.

A natural approach to predict a phenotype from metabolomic profiles expressed in the wavelet domain would then be to perform a thresholding prior to the application of a well chosen regression method (see, e.g., [Xia et al., 2007]). But this methodology does not link the wavelet coefficients selection to the prediction purpose. An alternative solution is to perform a variable selection method, that takes into account the target variable, before learning the regression or the classification function. In this direction, [Alexandrov et al., 2009] uses a multiple testing approach with a Benjamini & Hochberg adjustment to select the relevant wavelet coefficients in relation to a target factor variable before building a classification model (based on SVM) to predict it. [Saito et al., 2002] proposes to select the wavelet coefficients that maximize the Kullback-Leibler divergence between estimated densities obtained for the various levels of a factor target variable before learning a classification function on the basis of the selected coefficients. Also, [Jouan-Rimbaud et al., 1997] uses a “Relevant Component Extraction” that thresholds the less informative wavelet coefficients from a PLS between the spectra and a target variable of interest. These latter approaches explicitly focused on wavelet coefficients se-

lection but any feature selection method is expendable for such a task (see [Liu and Motoda, 1998, Guyon and Elisseeff, 2003] for reviews about feature selection). Feature selection algorithms can be time consuming and it has also been pointed out in [Raudys, 2006] that they can lead to feature *over*-selection that hinders the prediction performances.

Another approach is to simultaneously select the variables and optimize the prediction error: [Alsberg et al., 1998b] select the wavelet coefficients that minimize the cross validation error of a PLS regression. Model selection methods penalize the prediction error with a quantity depending on the number of variables involved in the regression (see, i.e., [Biau et al., 2005, Rossi and Villa, 2006] for examples in a similar framework where the signal is projected onto an orthogonal basis for classification purpose where the data are functions). However, model selection requires the definition of a relevant penalty term that can be hard to choose effectively, as pointed out in [Fromont and Tuleau, 2006].

3.2 A sparse one-phase approach

More recently, sparse methods [Tibshirani, 1996] have been intensively developed because they allow the selection of the relevant predictors during the learning process in an efficient and elegant way. The prediction error is penalized by the L^1 norm of the parameters of a linear model and it can be proved that this leads to nullify some of the parameters in an optimal way.

Our proposal is to use penalized regression methods to simultaneously

191 define a regression function and select the most important wavelet coefficients
 192 involved in the definition of this regression function. More precisely, the
 193 numerical variable of interest (here, the total HR dose ingested by the mice,
 194 $(y_i)_i$) is predicted from the metabolomic spectra through a penalized linear
 195 model where the predictors are all the wavelet coefficients (without prior
 196 thresholding). More precisely, the regression function Φ in Equation 1 is
 197 estimated by a penalized linear regression on the wavelet coefficients (used
 198 instead of X_i as predictor variables): $\hat{\phi}(W_i) = W_i^T \hat{\beta}$ where

$$\hat{\beta} = \arg \min_{\beta \in \mathbb{R}^D} \frac{1}{397} \sum_i \|y_i - W_i^T \beta\|_{\mathbb{R}^D}^2 + \lambda p(\beta)$$

199 where $\|z\|_{\mathbb{R}^D}^2 = \sum_{j=1}^D z_j^2$.

200 Depending on the form of the penalization, $p(\cdot)$, the method is likely to
 201 perform a rough or less rough variable selection:

- 202 • if $p(\beta) = \|\beta\|_{L^1} = \sum_{j=1}^D |\beta_j|$, the linear regression is a sparse linear
 203 regression also named LASSO [Tibshirani, 1996]. It selects wavelet
 204 coefficients, in the set of D original coefficients, in a optimal way for
 205 prediction purpose;
- 206 • if $p(\beta) = \|\beta\|_{\mathbb{R}^D}^2$, the linear regression is a ridge regression which tends
 207 to produce β with small norms but does not perform a selection of the
 208 wavelet coefficients;
- 209 • if $p(\beta) = (1 - \alpha)\|\beta\|_{\mathbb{R}^D}^2 + \alpha\|\beta\|_{L^1}$, $\alpha \in]0, 1[$ the linear regression is

210 the so-called “elasticnet” method [Zou and Hastie, 2005], proposed in
211 an attempt to use the advantages of the two previous penalties. As
212 LASSO, it selects a reduced number of wavelet coefficients involved in
213 the regression function but this number is usually larger than the one
214 obtained when using the LASSO method.

215 Using a sparse linear regression method, such as LASSO or elasticnet,
216 then leads to perform a thresholding that is adapted to the regression task.
217 Moreover, the thresholding is made in a joint way, leading to select a common
218 set of wavelet coefficients for all the spectra (contrary to standard threshold-
219 ing that nullify a different set of wavelet coefficients for each spectrum). This
220 property is likely to help prevent overfitting. Finally, sparse regressions lead
221 to the selection of a very limited number of coefficients that can, eventually,
222 help the interpretation (see Section 4 for a discussion and a comparison of the
223 different numbers of selected wavelet coefficients according to both methods).

224 **3.3 Comparison methodology**

225 The comparisons aim at understanding how the different approaches per-
226 forms in predicting the total dose of HR ingested by mice. Different wavelet
227 approximations and regression methods are combined. More precisely,

- 228 • the possible wavelet approximations applied to the pre-processed data
229 (as described in Section 2.2) are raw spectra (no wavelet approxima-
230 tion), wavelet coefficients (Haar or D4 bases), thresholded wavelet co-

231 efficients (D4), undecimated wavelet detailed coefficients (D4).
 232 “*thresholded wavelet coefficients*” correspond to the wavelet coefficients
 233 that remain positive after a soft threshold with SURE policy and “*un-*
 234 *decimated wavelet detailed coefficients*” correspond to the union of the
 235 finest details coefficients of the original spectra with the finest de-
 236 tails coefficients of the shifted spectra (obtained using the approach
 237 of [Beylkin, 1992, González et al., 2013]). When using the full wavelet
 238 decomposition or the “undecimated wavelet” approach, the dimension-
 239 ality of the original problem, $D = 751$ is left unchanged whereas the
 240 “thresholded wavelet” approach leads to a dimensionality reduction
 241 ($D = 71$ for D4 DWT), which is a standard way to handle large dimen-
 242 sion regression tasks.

- 243 • the possible regression method applied to the wavelet coefficients are
 244 sparse or regularized regression methods as described in Section 3.2
 245 (LASSO, ridge regression and elasticnet), PLS regression, which is a
 246 standard approach when dealing with a large number of variables and
 247 random forest [Breiman, 2001], as a basis for a comparison with non-
 248 linear methods.

249 For a sake of simplicity, only the following combinations are compared:

- 250 • any wavelet approximation is combined with the elasticnet regression.
 251 Our proposal is to use the full wavelet decomposition (without thresh-
 252 olding) with a sparse regression method. To enlighten the uselessness of

253 the thresholding when using a sparse regression method, thresholding
254 is also combined with elasticnet in the comparison;

- 255 • the full wavelet decomposition is also combined with any regression
256 method described above.

257 A total of 9 combinations are thus compared, summarized in Table 1.

258 [Table 1 about here.]

259 In order to train and to evaluate each of these combinations, the following
260 methodology is applied:

261 **Wavelet transform** First, the data are or are not preprocessed by a DWT.

262 The obtained coefficients are also scaled (each coefficient is centered to
263 a zero mean and scaled to a standard deviation equal to 1).

264 **Split** The observations (i.e., the pairs $(W_i, y_i)_i$) are randomly split into a
265 training set \mathcal{S}_T and a test set \mathcal{S}_V with balanced sizes (approximatively
266 200 observations each) taking into account the proportion of observa-
267 tions in the groups defined by sex, dose (including the control group
268 to train the regression function so that it can predict when the animal
269 is not affected by HR ingestion) and day of measure. To estimate the
270 methods variability, this step is repeated 250 times giving 250 training
271 sets and the corresponding test sets.

272 **Train** The regression method is then applied to each training set. Several
273 methods involve hyper-parameters that have to be tuned: for random

274 forest, the hyper-parameters are the number of trees, the number of
 275 variables selected for a given split, ... They are set to the default val-
 276 ues, coming from useful heuristics; the stabilization of the out-of-bag
 277 error is achieved using that strategy.

278 For sparse and regularized linear regressions, an optimal λ is auto-
 279 matically selected through a regularization path algorithm (see, e.g.,
 280 [Efron et al., 2004] for the LARS algorithm in the case of LASSO).
 281 Additionally, for elasticnet, the mixing coefficient α is set to 0.5 which
 282 was the best choice according to other experiments in which α was
 283 varied in $\{0.1, 0.25, 0.5, 0.75\}$ (not shown in this paper for a sake of
 284 simplicity).

285 Finally, for PLS, the number of kept components (between 1 and 40) is
 286 tuned by a 10-fold cross-validation strategy performed on the training
 287 set.

288 **Test** The root mean square error (RMSE) is calculated for each approach
 289 involved in the comparison and for all the corresponding test sets:

$$RMSE_V = \sqrt{\frac{1}{n_V} \sum_{i \in \mathcal{S}_V} (y_i - \hat{y}_i)^2}$$

290 where n_V is the number of observations in the test set and \hat{y}_i is the
 291 estimation of the total dose of HR ingested.

292 The methodology described above is illustrated in Figure 2. It leads to
 293 obtain nine sets of 250 test errors, one for each combination of a wavelet

294 transform and regression algorithm.

295 [Figure 2 about here.]

296 All the simulations are performed using **R** free software
297 [R Development Core Team, 2012] and the packages **wavethresh**
298 [Nason and Silverman, 1994] (for wavelet facilities), **glmnet**
299 [Zou and Hastie, 2005] (for sparse and regularized linear methods), **mixOmics**
300 [Lê Cao et al., 2009] (for PLS) and **randomForest** [Liaw and Wiener, 2002]
301 (for random forest).

302 4 Results and discussion

303 This section presents the results of the experiments described in Section 3.
304 Section 4.1 is devoted to the comparison of the numerical performances of
305 the various combinations. The differences between the approaches (including
306 the number of wavelet coefficients selected) are discussed. Then, Section 4.2
307 extracts relevant features from the best combination of wavelet preprocessed
308 and regression method and compares it with a previously known list. This
309 provides another point of view on the relevance of the combination of the
310 DWT with sparse and regularized linear models for metabolomic data anal-
311 ysis, this time as a feature selection method. The biomarkers that are the
312 most involved in the prediction of the total dose of HR ingested are selected
313 using an importance measure. The overall methodology is general enough to
314 be expandable for any regression method.

315 4.1 Numerical performances comparison

316 The averaged RMSE over the 250 test sets as well as their standard deviations
317 are reported in Table 2.

318 [Table 2 about here.]

319 In addition, the boxplot of the R^2 over the 250 test sets¹ are given in
320 Figure 3 for the case where the data are expanded on the D4 basis and
321 where all wavelet coefficients are kept.

322 [Figure 3 about here.]

323 For the best method (combination of a DWT on a D4 basis with elasticnet),
324 the mean R^2 is equal to 89.00% which is quite satisfactory. Thus, the ac-
325 curacy of the prediction on the sample test is good enough to be used as
326 a relevant method to estimate the total dose of HR ingested by the animal
327 from the metabolomic profile alone.

328 Conversely, being able to predict the HR ingestion from the metabolomic
329 profile is a proof that the disrupting effect of HR on the metabolism is not an
330 artefact because an accurate relation between both variables is established.
331 Contrary to a test approach, that would have lead to test each part of the
332 metabolomic profile, this approach enlighten the strength of the relation
333 between the whole metabolomic spectrum and the target variable, here the
334 HR dose. Moreover, it does not even require the use of a control group.

$$^1 R^2 = 1 - \frac{\sum_{i=1}^{n_{\text{Test}}} (y_i - \hat{y}_i)^2}{\sum_{i=1}^{n_{\text{Test}}} (y_i - \bar{y})^2} \text{ where } \bar{y} = \frac{1}{n_{\text{Test}}} \sum_{i=1}^{n_{\text{Test}}} y_i.$$

335 4.1.1 Comparison of the wavelet transforms

336 The first conclusion arising from Table 2 is that the wavelet transform effect
337 is stronger than the choice of the regression method. In particular, using the
338 wavelet coefficients remaining after a soft thresholding results in less accurate
339 predictions than using all the wavelet coefficients or even than the direct use
340 of the raw data.

341 Moreover, using all the wavelet coefficients in combination with a sparse
342 approach (elasticnet or LASSO) is the most accurate method; the impact
343 of the basis choice (D4 or Haar) is almost negligible. Undecimated wavelet
344 transform is the second most accurate wavelet transform approach: this may
345 be the indication that the coefficients with the finest details contain most
346 of the useful information for the prediction task. Maybe, an optimal trade-
347 off would be to select wavelet coefficients at several scales, leaving only the
348 coefficients at the crudest scales.

349 To assess the significance of these conclusions, paired t-test were com-
350 puted to compare the RMSE of the various wavelet transforms: the differ-
351 ences between the use of Haar or D4 wavelets are not significant (at level
352 1%) but the differences between the use of all D4 wavelet coefficients and the
353 use of either the raw spectra, the D4 undecimated wavelet approach or the
354 D4 thresholded coefficients are all significant. Note that, even if the differ-
355 ences between the averaged RMSE seem to be small, they are calculated over
356 250 replica which is a large enough number to provide confidence in these
357 conclusions.

358 4.1.2 Comparison of the regression methods

359 Comparing the regression methods, those that are (at least partially) based
360 on a sparse regularization, such as elasticnet and LASSO, obtain the best
361 results. Ridge regression is not as accurate as the methods based on a sparse
362 regularization but its variability is lower. Actually, combining a ridge and a
363 sparse penalty in the elasticnet seems to slightly decrease the variability of
364 the elasticnet results compared to those of the LASSO (except for two outlier
365 samples). Moreover, the influence of the mixing parameter α is not really
366 strong: test errors for elasticnet with $\alpha = 0.1$, 0.25 or 0.75 are not shown in
367 the paper but would have mostly lead to the same conclusion: $\alpha = 0.1$ or
368 0.25 has slightly deteriorated (but comparable) test errors, whereas $\alpha = 0.75$
369 has test errors closer to the LASSO.

370 Finally, PLS, that is probably better suited for explanatory purpose, does
371 not give very satisfactory predictive performances in this case study but also
372 has a low variability. Here, random forest is the method that gives the worst
373 accuracy and also the largest variability of the performances over the 250
374 test sets.

375 Once again, the significance of these conclusions can be assessed by paired
376 t-tests: the differences between RMSE obtained by elasticnet and RMSE
377 obtained by ridge regression are significant. Of course, the same remark holds
378 for the comparison between elasticnet and any method performing worse
379 than ridge regression. This leads to the conclusion that the combination of a
380 DWT and a sparse linear method, such as elasticnet, is indeed a good choice

381 to handle regression problems where the predictors are metabolomic data.

382 **4.1.3 Number of selected wavelet coefficients**

383 Section 3.2 explains that using a sparse method on all the wavelet coefficients
384 can be seen as a joint thresholding adapted to the target variable. Then, it is
385 interesting to compare the numbers of coefficients selected by sparse methods
386 to the number of coefficients selected by a classical thresholding approach.
387 For D4 basis, 71 wavelet coefficients remain after the soft thresholding phase.
388 The numbers of selected coefficients over the 250 regression functions pro-
389 vided by elasticnet and lasso are given in figure 4.

390 [Figure 4 about here.]

391 The average number of selected coefficients is often much smaller than the
392 one obtained with the classical thresholding approach. For instance, the best
393 method (elasticnet) selects 46.5 wavelet coefficients on average. Hence, not
394 only are the “one-phase” approaches faster and more accurate, they also
395 select less (but more relevant, according to the increase in accuracy) wavelet
396 coefficients.

397 **4.2 Important biomarkers extraction**

398 The relevance of the application of elasticnet on all the wavelets coefficients
399 is assessed by using the learned regression function, obtained in the previous
400 section, in order to extract the most important features related to the total

401 dose of HR ingested. A natural approach would be to directly analyze the
402 variables selected by the sparse regression but, because of the wavelet trans-
403 form preprocessing, these are not directly linked to the spectra locations that
404 are of interest.

405 Alternatively, a standard approach, for linear models, is to select the
406 most important variables by the p-values of the coefficients associated to
407 the variables; this approach is not reliable in our context, both because it
408 only selects the most important wavelet coefficients (and, once again, not the
409 spectra locations) and also because if the explanatory variables are highly
410 correlated, the results of such tests are strongly related to the variables that
411 are used in the model. A small change in the list of explanatory variables
412 can lead to a very different list of significant variables and thus, the approach
413 is not really reliable in the case of a large number of explanatory variables.

414 To overcome these difficulties and to achieve the study of the influence
415 of the original variables (and not of the wavelet coefficients) in the predic-
416 tion, we used a generalization of the importance measure originally designed
417 for random forest [Breiman, 2001]. This approach provides a way to assess
418 the relevance of biomarkers, to quantify their respective implications in the
419 biological phenomenon and thus to corroborate a list of biomarkers already
420 extracted elsewhere. In the following, Section 4.2.1 describes our approach
421 whereas Section 4.2.2 analyzes the results.

4.2.1 A measure of the importance of the variables

L. Breiman proposes the calculus of an “importance” measure to assess the relevance of each explanatory variable in a random forest [Breiman, 2001]. This measure is based on the observations that are not used to train a given tree (out-of-bag observations): the values of the explanatory variable under study are randomly permuted and the importance is defined as the decrease of the accuracy (in terms of increased mean square error for a regression problem) between the predictions made with the real values and those made with the randomly permuted values. The more the MSE increases, the more important the variable is for prediction. This approach was proven to be successful in variable selection in [Archer and Kimes, 2008, Genuer et al., 2010].

We propose to use a similar approach to describe the way a wrong value for a given variable (here a given value in the spectrum) propagates through the wavelet transform and the regression function and affects the accuracy of the final prediction of the total dose of HR ingested by the mouse. This analysis is focused on the best regression approach, i.e., the use of all wavelet coefficients coming from a D4 basis expansion combined with elasticnet. As in the approach proposed in [Breiman, 2001], the importance is calculated from observations that are not used during the training process. More precisely, the 250 test samples described in Section 3.3 are used to calculate importance measures: the “importance” of a variable is the mean rate (over the test sets) of MSE increase after a random permutation of its values among the individuals (the other variables remaining with their true values). The idea

445 is to assess the prediction power of a variable by means of the prediction
 446 accuracy disruption when this variable is given false values. The process is
 447 repeated for the 751 variables corresponding to spectra locations, as described
 in Algorithm 1. It can handle the way a given part of the spectra affects the

Algorithm 1 Variables importance calculation

- 1: **for** each explanatory variable, v of the data set **do** {Variable loop}
 - 2: **Randomization** Randomize the values of v for the 397 observations.
 The new explanatory variables (spectra) with randomized values for v
 are denoted by $(X_i^v)_i$;
 - 3: **Wavelet expansion** Calculate the wavelet coefficients with a D4 ex-
 pansion for $(X_i^v)_i$. These are denoted by $(W_i^v)_i$;
 - 4: **for** each test set, \mathcal{S}_V **do** {Test set loop}
 - 5: **Mean square error calculation** Calculate the MSE based on the
 explanatory variables $(W_i^v)_{i \in \mathcal{S}_V}$, $\text{MSE}_{v, \mathcal{S}_V}$;
 - 6: **Importance calculation for \mathcal{S}_V** Compare $\text{MSE}_{v, \mathcal{S}_V}$ to the original
 MSE obtained for the test set \mathcal{S}_V , $\mathcal{I}_{v, \mathcal{S}_V} = 1 - \frac{\text{MSE}_{\mathcal{S}_V}}{\text{MSE}_{v, \mathcal{S}_V}}$;
 - 7: **end for**
 - 8: **Importance calculation for variable v** Average over the $T = 250$
 test samples: $\mathcal{I}_v = \frac{\sum_{\text{Test sets}} \mathcal{I}_{v, \mathcal{S}_V}}{T}$.
 - 9: **end for**
-

448
 449 quality of the prediction of the total dose of HR ingested. It thus gives an
 450 assessment to the most relevant features in metabolomic spectra (i.e., the
 451 features that contribute the most to an accurate prediction of the HR dose),
 452 despite the series of transformations done.

453 4.2.2 Results of the biomarkers extraction and comments

454 Figure 5 gives the importance of the 751 original variables (spectra locations)
 455 ranked by decreasing value.

456

[Figure 5 about here.]

457 One variable is clearly much more important than all the other ones because
458 random permutations of its values cause an increase of almost 80% in MSE.
459 Three other variables seem to be important (with importance greater than
460 20%) and another group of 5 variables are also important to a lesser extent
461 (between the yellow line and the orange line in Figure 5).

462 The list of the “most important” spectra locations and the names of the
463 associated metabolites (when it is known) are given in Table 3. Moreover,
464 the location of these metabolites in a ^1H NMR spectrum is shown in Figure 6.

465

[Table 3 about here.]

466

[Figure 6 about here.]

467 The most important metabolite is the *scyllo*-inositol which was also identified
468 as an important metabolite in [Domange et al., 2008]. The other metabolites
469 emphasized by the variable importance (creatinine, hippurate, valine) were
470 also present in the original work: this confirms the reliability of our proposal.
471 Other spectra locations, that do not correspond to known metabolites, are
472 also identified by the variable importance. Noticing the relevance of the
473 most important metabolites found by our approach, these unknown peaks are
474 indications for further biological analysis to find new metabolites involved in
475 the poisoning process.

476 Also, some differences arise when comparing this list with the list
477 of biomarkers identified in [Domange et al., 2008]. Part of these dif-

478 ferences may be explained by the fact that the dependent variable in
 479 [Domange et al., 2008] is the daily HR dose ingested (i.e., a factor variable
 480 with 3 levels) whereas, here, the total ingested dose was used in order to take
 481 into account the cumulative effect of the ingestion. But it is also the positive
 482 counterpart of not using a test approach and thus avoiding the standard false
 483 positive issue that comes with them. As the extracted spectra locations are
 484 directly related to the quality of the prediction, they are more reliable, even
 485 if not so well theoretically justified.

486 Finally, not only does this approach give a list of important spectra lo-
 487 cations (corresponding to the total dose of HR ingested) but it also provides
 488 a quantification of the influence of the spectra location on the accuracy of
 489 the prediction. In our problem, *scyllo*-inositol therefore appears as the most
 490 important metabolite affected by HR ingestion because its randomization
 491 causes an 80% increase of the average MSE.

492 **5 Conclusion**

493 Wavelet transformation is commonly used to deal with spectrometric data in
 494 biology, especially for de-noising purposes. Moreover, this paper shows that,
 495 associated with a convenient learning method, it improves the understanding
 496 of the relation between metabolomic spectrum and a phenomenon of interest
 497 (for instance, metabolic disruptions linked to HR ingestion). It is also shown
 498 that using a de-noising approach, not related to the variable to be predicted,

499 can lead to a dramatic loss of information. More precisely, some important
500 variables seem to be located in parts of the spectra that could be seen as
501 “minor” details. It is thus important to combine the wavelet transform and
502 de-noising with the purpose of the study. Sparse methods, that combine
503 a regression model and a variable selection seem to be well suited to this
504 task: they perform a kind of joint thresholding of the wavelet coefficients
505 that is directly related to the target variable. In particular, elasticnet gave
506 the best performance in prediction and was also able to provide a relevant
507 list of biomarkers, linked to the target variable, in our case study.

508 In conclusion, the combination of DWT with elasticnet can be used to ac-
509 curately predict a numerical variable of interest from the metabolomic profile.
510 It is also useful to identify and confirm the most important features involved
511 in the biological process under study thanks to the importance measure in-
512 troduced in this article.

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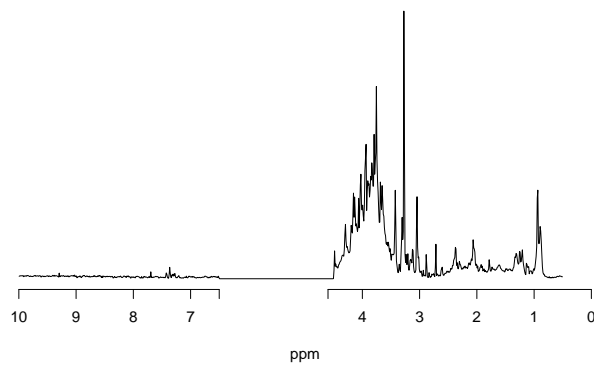


Figure 1: An example of metabolomic spectra from data discussed in Section 2 (female mice of the control group at day 0).

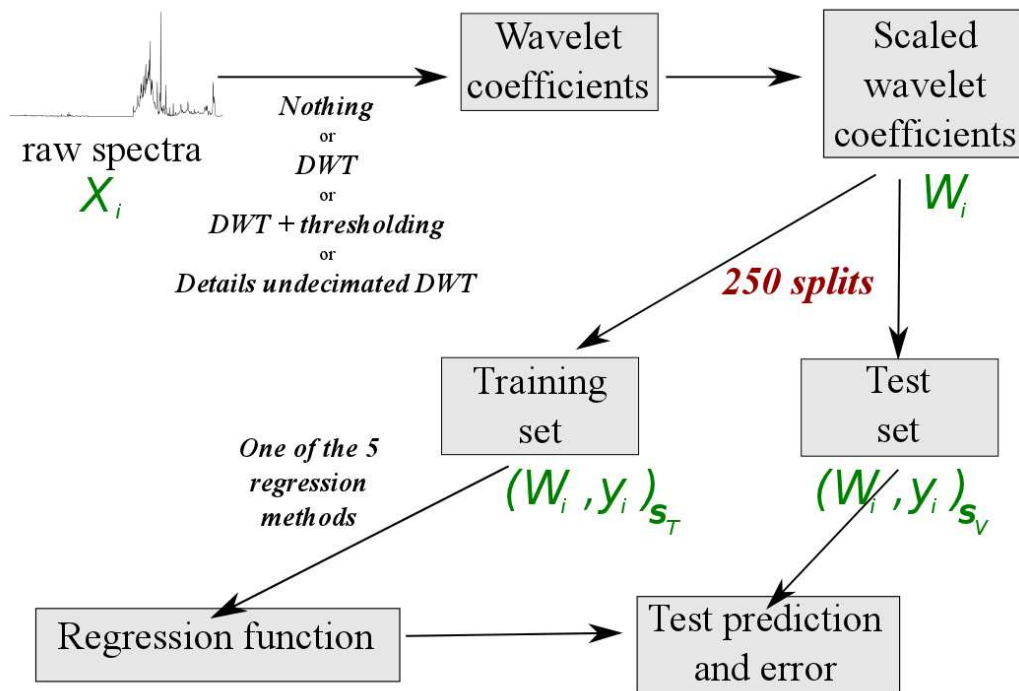


Figure 2: Illustration of the methodology used to compare various combinations of wavelet transforms and regression methods

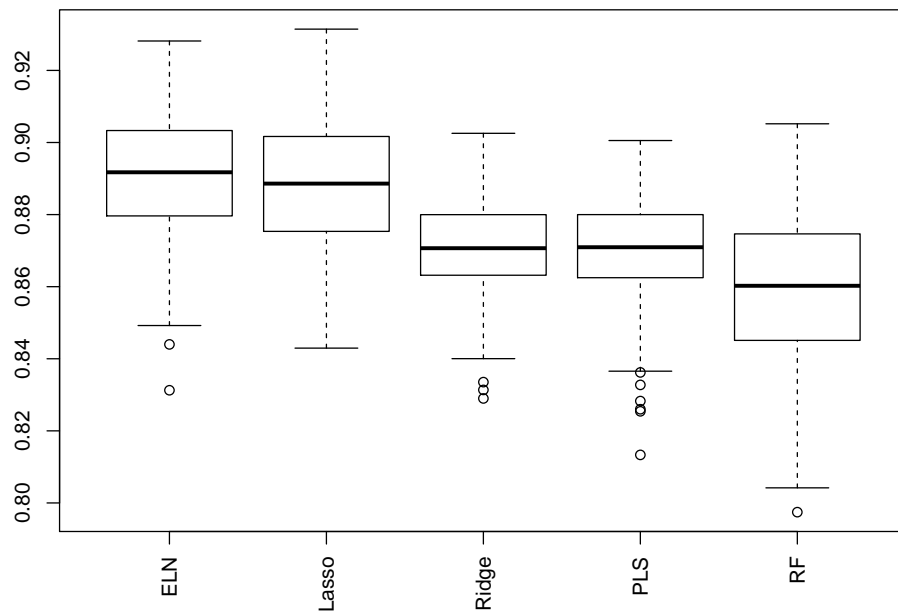


Figure 3: Boxplots of the R^2 of the mean square errors over the 250 test sets for the prediction of the total dose of HR ingested with various learning methods and a full representation with D4 wavelets.

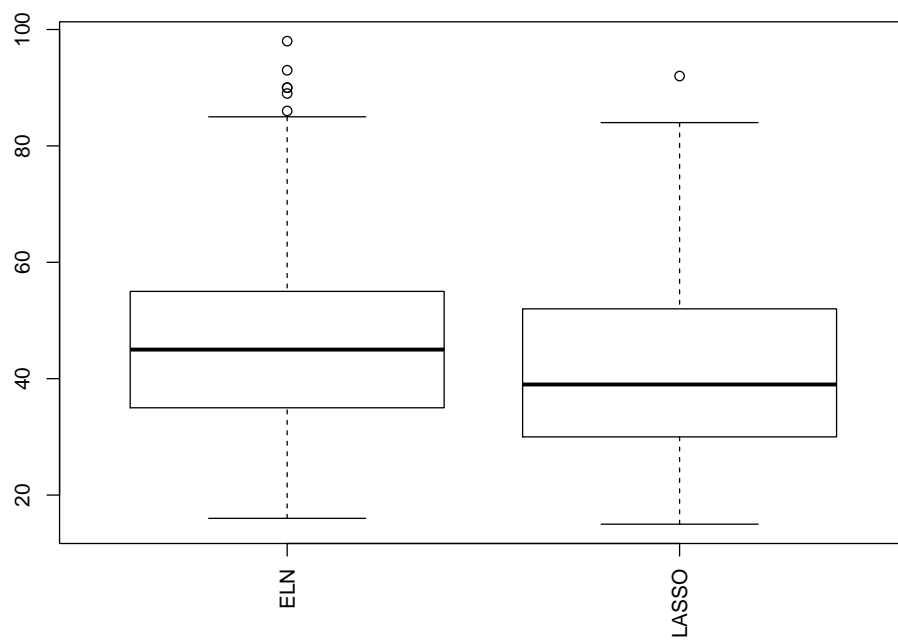


Figure 4: Number of wavelet coefficients selected by elasticnet (ELN) and LASSO over the 250 train sets for D4 wavelet expansion using all the coefficients

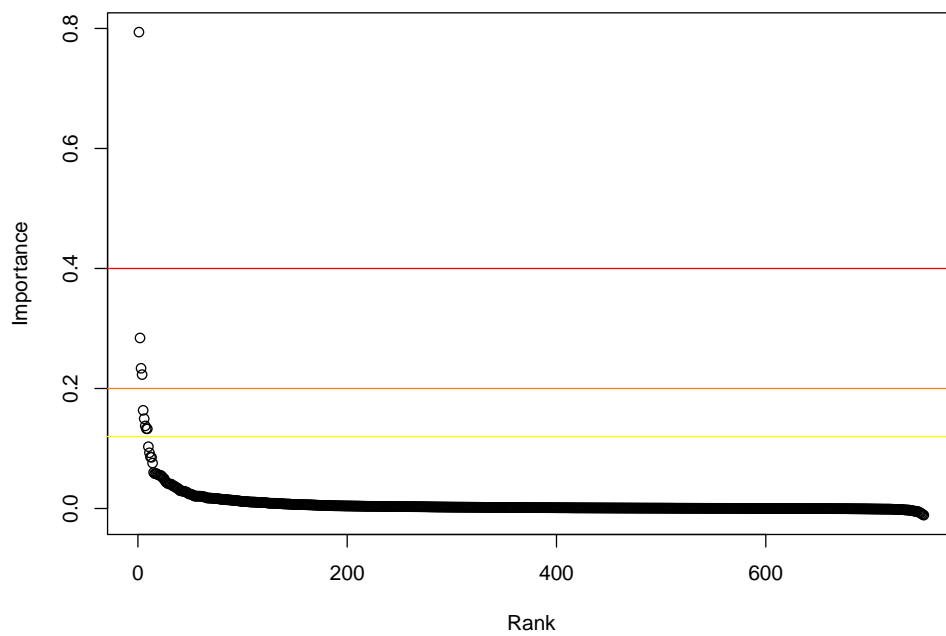


Figure 5: Importance of the 751 spectral locations ranked by decreasing value. The horizontal lines separate increasing degrees of importance from above the red line (very important) to below the yellow line (not important).

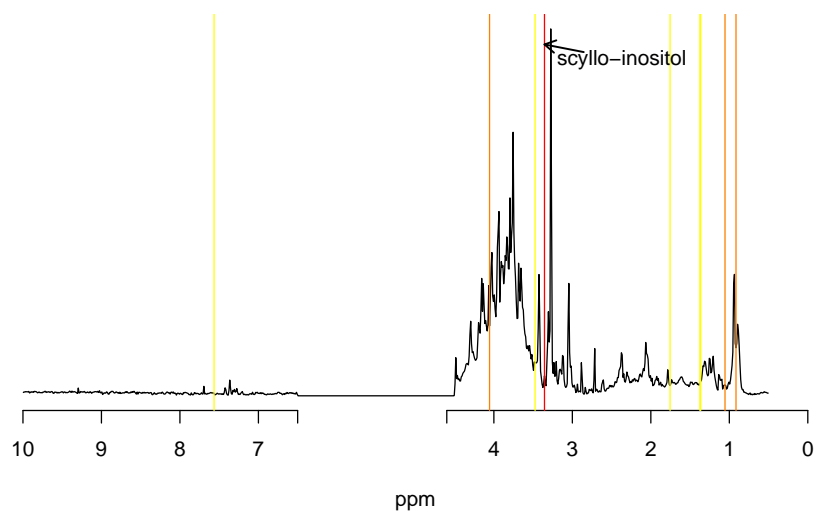


Figure 6: “Most important” metabolites locations on the ^1H NMR spectra for the prediction of the total dose of HR ingested by the mouse. The colors correspond to those of Figure 5.

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DWT	Wavelet basis	Regression method
raw spectra	\propto	ELN (elasticnet)
full wavelets	Haar	ELN
full wavelets	D4	ELN
undecimated wavelets	D4	ELN
thresholded wavelets	D4	ELN
full wavelets	D4	LASSO
full wavelets	D4	Ridge
full wavelets	D4	PLS
full wavelets	D4	RF

Table 1: Approaches (wavelet transform and pre-processing combined with a regression method) compared to predict the total HR ingestion from the metabolomic profiles.

Wavelet transform	Regression method	average RMSE	sd RMSE
Raw spectra	ELN	16.3	1.0
full wavelets (D4)	ELN	14.3	1.1
undecimated wavelets (D4)	ELN	15.4	0.9
thresholded wavelets (D4)	ELN	42.9	52.3
full wavelets (Haar)	ELN	14.5	1.0
full wavelets (D4)	LASSO	14.5	1.1
full wavelets (D4)	Ridge	15.6	0.7
full wavelets (D4)	PLS	15.6	0.9
full wavelets (D4)	RF	16.2	1.2

Table 2: Means and standard deviations of root mean squared errors for the prediction of the total dose of HR ingested with various combinations of wavelet transforms and regression methods. “ELN” means “elasticnet”; “Ridge” means “ridge regression”; “RF” means “random forest”; “D4” means “Daubechies 4 wavelet basis” and “Haar” means “Haar wavelet basis”. Bold capitals are used to emphasize to the best method among all experiments.

ppm	Importance	Metabolites	Change with HR
3.35	79.4%	<i>scyllo</i> -inositol	↗
4.05	28.4%	creatinine	↘
1.05	23.4%	valine	↗
0.91	22.3%	unassigned	↘
1.37	16.4%	unassigned	↗
1.36	15.0%	unassigned	↗
7.56	13.8%	hippurate	↗
3.47	13.3%	unassigned	↘
1.75	13.3%	unassigned	↗

Table 3: Summary of the “most important” peaks (and, if known, metabolites) for the prediction of the total dose of HR ingested by the mouse.